

GenCore version 5.1.4_p5_4578
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_P2n model

Run on: April 5, 2003, 02:50:22 ; Search time 1526 Seconds

(without alignments)
 4669.734 Million cell updates/sec

Title: US-09-847-081B-2

Perfect score: 2270

Sequence: 1 MMSVALLWVSPSTSEVSNG.....IAYAKSLVPPNRTSSPLAKT 440

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summariesCommand line parameters:
 -MODEL=frame+P2n,model -DEV=xIP
 -O=/cgn2_1/USPTO_spool/us09847081/runat_01042003_120129_26749/app-query.fasta_1..583
 -DB=EST -QFORMAT=fasta -MATCH=0..1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=-1 -END=-1 -TRANS=human40 cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGNN=15 -MODE=LOCAL
 -OUTFILE=pto -NORM=EXT -MAXLEN=2000000000
 -USER=US09847081 -eGNUM=1..1..2874 -eRUNAT=120129_26749 -NCPU=6 -ICPU=3
 -NO_XLIPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELETE=7

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpi:*

7: em_htc:*

8: em_estro:*

9: gb_est1:*

10: gb_est2:*

11: qb_htc:*

12: qb_est3:*

13: qb_est4:*

14: qb_est5:*

15: em_estfun:*

16: em_estom:*

17: qb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_Plh:*

21: em_gss_vrt:*

22: em_grs_fun:*

23: em_grs_man:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1211	53.3	165	11 AY11032	Zea mays
2	1202	53.0	787	13 BM410846	BM410846 EST585173
3	1201.5	52.9	1201	11 AY10547	Zea mays
C	4	1179	51.9	781	B0511016 EST618431
	5	1136	50.0	751	B0046203 EST595321
	6	1130	49.8	765	13 BM408984 EST583311
	7	1099	48.4	686	10 AY442101
	8	1083	47.7	682	13 BM409200
	9	1072	47.2	672	10 AW442407
	10	1049	46.2	642	10 BE433118 EST39722
	11	1043	45.9	676	10 AW22027 EST59838
	12	1001	44.1	677	12 BG151357
	13	997	43.9	634	13 BM412533 EST586860
	14	980	43.2	600	10 BE460889 EST412308
	15	977.5	43.1	623	10 BE432511 EST399040
	16	956	42.1	685	10 AW221932 EST298743
	17	947	41.7	582	10 AW223316 EST30127
	18	940	41.4	581	10 BM32955 EST39484
	19	939	41.4	623	13 BM536249 EST589271
	20	934	41.1	582	10 AW23666 EST30477
	21	927	40.8	744	13 BM412719 EST587057
	22	921	40.6	562	10 BE433966 EST3044
	23	921	40.6	562	10 BE433966 WHE2629_C
	24	918	40.4	634	13 BM137086 EST39124
	25	917	40.4	565	10 BE432508 EST39124
	26	916	40.4	573	10 BE435308 EST39124
	27	913	40.2	585	10 AW222245 EST299056
	28	907	40.0	668	13 BM955682 HVSME002
	29	899	39.6	556	10 AW22152 EST598963
	30	891	39.5	609	10 BE222877 NF048H111
	31	891	39.3	581	10 AW222806 EST299612
	32	884	38.9	645	10 AW496851 9a:9b02..Y
C	33	884	38.9	791	10 AW223528 EST303339
	34	881	38.8	542	10 BE431550 EST136365
	35	879	38.7	613	13 B1957464 HVSNEN000
	36	877	38.6	543	13 BM411875 EST586202
	37	873	38.5	634	10 AW441216 EST310612
	38	873	38.5	687	10 BE44578 EST305656
	39	870	38.3	542	10 BE432748 EST399277
	40	867	38.2	563	10 BE461396 EST412815
	41	865	38.1	555	10 BE460463 EST411882
	42	860	37.9	566	12 BF112979 EST440662
	43	858	37.9	536	10 BE4334911 EST405989
	44	856	37.7	563	10 BE437095 EST408213
	45	848	37.4	551	10 BE432084 EST398613

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	mRNA sequence
AY11032	AY11032	Zea mays CL1906..1	
ACCESSION	AY11032	VERSION	HTC..
KEYWORDS		SOURCE	Zea mays
ORGANISM			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	Haines, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Morgante, M., and Tingey, S.V.	1 (bases 1 to 1655)	
AUTHORS	Arthur, L.W.		

Site 2: XbaI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp.

BASE COUNT 230 a ORIGIN 211 g 214 t

	LOCUS AY108547	1201 bp	mRNA	linear	HTC 25-MAY-2002
	DEFINITION Zea mays PC0131047 mRNA sequence.				
	ACCESSION AY108547				
	VERSION AY108547.1				
	KEYWORDS HTC.				
	SOURCE Zea mays				
	ORGANISM Zea mays				
	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
	REFERENCE 1 (bases 1 to 1201)				
	AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgan, M. and Tingey, S.V.				
	TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overio Probes				
	JOURNAL Unpublished (2002)				
	REFERENCE 2 (bases 1 to 1201)				
	AUTHORS Coe, E.C.				
	TITLE Direct Submission				
	JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
	FEATURES Location/Qualifiers				
	source 1..1201				
	/organism="Zea mays"				
	/clone_xref="MaizeDB:637648"				
	/db_xref="taxon:577"				
	/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"				
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"				
	BASE COUNT 273 a	325 c	316 g	287 t	
	ORIGIN				
	Alignment Scores:				
Pred. No.:	Pred. No. :	1.56e-137	Length:		
Score:	Score:	1201.50	Matches:	223	
Percent Similarity:	Percent Similarity:	92.92%	Conservative:	28	
Best Local Similarity:	Best Local Similarity:	82.29%	Mismatches:	19	
Query Match:	Query Match:	52.93%	Indels:	1	
DB:	DB:	11	Gaps:	1	
	US-09-847-081B-2 (1-440) x AY108547 (1-1201)				
Qy	185 ArgThrAspGluLeuValAspGLYProAsnAlaSerHisIleThrProGlnAlaLeuAsp	204			
Db	307 AGAACAGTGAACATTGTGATGCCAAACGATCATATACTACCGCAATTAGAT	366			
Qy	205 ArgTrpGluIleArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAla	224			
Db	367 AGCTGGAAATTAGGGTAGAAGATGTTCAATGGCCATTATGGCATATATGGTCAGA	306			
Qy	188 ArgThrAspGluLeuValAspGLYProAsnAlaSerHisIleThrProGlnAlaLeuAsp	204			
Db	307 AGAACAGTGAACATTGTGATGCCAAACGATCATATACTACCGCAATTAGAT	366			
Qy	205 ArgTrpGluIleArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAla	224			
Db	367 AGCTGGAAATTAGGGTAGAAGATGTTCAATGGCCATTATGGCATATATGGTCAGA	306			
Qy	225 AlaLeuSerAspThrValAspIlePheSerArgTyrosylsThrPheAspGluLeuTyIleLeu	244			
Db	427 GCCTTGTCGATACAGTTCTAACCTTCAGTGTATTCAGCATAGATACTT	486			
Qy	245 GluGlyMetArgMetAspLeuThrPheSerArgTyrosylsThrPheAspGluLeuTyIleLeu	264			
Db	487 GAAGGAAGGCGTATGGACTTGAGAAATCGAGATAAACACTTCAGAAACTATACCTT	546			
Qy	265 TyrCystYrrValAlaGlyIleGluMetSerValProValMetGlyIleAla	284			
Db	547 TATGTGTTATTATGTTGGTGTAGGTGTTGGTATGGCTATGGCTGTGGGATGCGA	606			
Qy	285 ProGluSerLysIleThrGluSerValTyAsnAlaAlaLeuAlaLeuGlyLeuAla	304			
Db	607 CCTCAATTAAGCCAACACAGAGGCTATAATGCTGCCTGTGGGATGCGA	666			
Qy	305 AsnGlnLeuThrAsnIleLeuArgAspValGlyGluAlaArgArgValTy	324			
Db	667 AACCATTAATCTACATCTACAGATTTGGAAATGGTGCAGAAGAGAGTCAC	726			
Qy	325 LeuProGlnAspGluLeuAlaGlnAlaGlyIleLeuSerAspGluAspIlePheAlaGlyArg	344			
Db	727 TTGCCCTCAGATGATTAGCACAGGAGTCTACTGCTACTAGTCAGCTGCCTATGACGTGGCC	786			
RESULT 3	AY108547				

infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes

LOCUS	527 GTCATGGCATGCCACTCCAGGCTGCACCAAGGCTGACATGCTGCTCTG 586	BASE COUNT	202 a - 191 c - 144 g - 244 t
DEFINITION	300 AlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArg 319	ORIGIN	
ORGANISM	587 GCTCAGCGCATCGCTAACAGCGTACGAGTATCTCAGGACGTRGGGGAAATGGCAGG 646	ALIGNMENT SCORES:	
REFERENCE	320 ArgGlyArgValtyLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339	Pred. No.:	4.78e-135
AUTHORS	647 AGGGGAGATAATACCTTCGTTGACGGCTTGCGAGCAGTCAGGAGAGAAC 706	Score:	1.179.
TITLE	340 IlePheAlaGlyArgValthrAspLysPArgAsnPheMetLysLysGlnIleGlnArg 359	Percent Similarity:	96.36%
JOURNAL	707 ATATCAGGGAAAGTGAACGGCAAGTGAGGGTTATGAGGGCAAGATCCAGGT 766	Best Local Similarity:	93.12%
COMMENT	QY 360 AlaArgLysPhePheAspGluSerGluIysGlyValIysGlyLeuAspSerAlaSerArg 379	Mismatches:	9
KEYWORDS	Db 767 GCCAGCGCTCTCGTGTGATGGCGAGAAGGGCTCACCCATCTCGACTCTGAGCAG 826	Indels:	1
SEQUENCE	QY 380 TrpProValLeuThrAlaLeuLeuItyArgLysIleLeuAspGluIysGluAlaAsn 399	Gaps:	0
OTHER_SRS:	Db 827 TGGCGGTGTCGTCGGCTCTGGCTGTGACGGAGATCTGTCGATTCAGGCAAC 886	US-09-847-081b-2 (1-440) x B0511016 (1-781)	
COMMENT	QY 400 AspTyAspAsnPheThrArgArgAlaThrValSerIleLeuThrLeu 419	QY 194 AsnAlaSerHistidLeuProGlnAlaLeuAspArgTrpAluThrArgLeuGluAspIle 213	
KEYWORDS	Db 887 GACTACAACATTCACCAAGCTGATGTCGCAAGCTGCGTA 946	Db 781 AATGATCAACATCACACATCACACTCCACAGCTTAGATAGTGGGAGGCCAGGATAT - 723	
OTHER_SRS:	QY 420 ProIleAlaItyAlaLysSerLeuValProPro 430	QY 214 PheSerGlyArgProPheAspPheMetLeuAspAlaAlaLeuSerAspThrValSerArgPhe 233	
COMMENT	Db 947 CCGCTGCTATATGCAAGGCTGCGCTGGTGGACCA 979	Db 722 TTCAACGGCGGGCATTTCATGATATGCTTGATGCAAGTACTGTTCCAAATT 663	
RESULT 4	B0511016/c	QY 234 ProValAspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeutTrpLys 253	
LOCUS	B0511016 781 bp mRNA linear EST 22-JUL-2002	Db 662 CCTCTGATTTCACTTCACCATTCAGTGGATGAGATGGATGGAA 603	
DEFINITION	EST61831 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMH067 3', end, mRNA sequence.	QY 254 SerArgTyLyStPheAspGluIeutTrLeutTyCystTyTyValAlaGlyThrVal 273	
ACCESSION	B0511016.2 GI:21926690	Db 602 TCCAGATAACACACTTGATGAACTATCTATTTGTTACTATGTCGTTGTCAGCA 543	
VERSION	EST	QY 274 GlyLeuMetSerValProValMetGlyIleLeuIapGluSerLysAlaIthThrGluSer 293	
KEYWORDS	Solanum tuberosum	Db 542 GGATTGATAGTGTTCCAATTATGGCATTGCACTGAACTCAANGCCAAGCAGAGT 483	
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I; Solanaeace; Solanum.	QY 294 ValItyAsnAlaLeuAlaLeuIaLenglyLeuAlaAsnGlnLeuThrAsnIleLeuIleuArgAsp 313	
ORGANISM	1 (bases 1 to 781)	Db 482 GTATATAAGCAGTTTGCCTTTGCCTTGGATGCTAGTACTACCAATACTACTAGAT 423	
REFERENCE	Buell,C.R., Hart,A., Baker,B., Tankle,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karamycheva,S.A.	QY 314 ValGlyGluAspAlaArgArgGlyIaArgValtyIleuProGlnAspGluLeuAlaGlnAla 333	
AUTHORS	Karamycheva,S.A.	Db 422 GTAGCAGAAATGCAAGAAAGATACTACCTCAAGATGAATTAGCAAGGCCA 363	
TITLE	Generation of a set of potato cDNA clones for microarray analyses	QY 334 GlyLeuSerAspGluAspIlePhenylAlaGlyArgValIthAspLysTrpArgAsnIshMet 353	
JOURNAL	Unpublished (2002)	Db 362 GGGCTCTCGATGAAAGACATTTCTGCTGAAGAGTACATGCTGGGATCTTTATG 303	
COMMENT	On Jun 10, 2002 this sequence version replaced 91:21369885.	QY 354 LysLysGlnIleGinArgAlaArgLysPheAspGluSerGluLysGlyIvaIthRglu 373	
KEYWORDS	Other_SRS: BSR618430	Db 302 RAGAGCAGATTCAAGGCCAGAAATCTTGTGAGCAGAAAAGGTGTCAAGAA 243	
ORGANISM	The Institute for Genomic Research	QY 374 LysAspSerAlaSerArgTrpProValLeuThrAlaLeuLeuLeuItyArgLysIleLeu 393	
REFERENCE	9712 Medical Center Dr, Rockville, MD 20850, USA	Db 242 CTGAGCTCGCTACTAGATGTCGCTGTTGTCGTTATGCCAAGTACTG 183	
AUTHORS	Contact: Robin Buell	QY 394 ASPAluIleGluAlaAsnAspPheAsnAsnAspPheThrArgGlnItyValSerIysPro 413	
TITLE	This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or cna@ergen.com	Db 182 GACCGATGTAAGGGAACTACRAACAACTTCNOAAGGGCTATGTGAGCAGCCA 123	
JOURNAL	Seq Primer: T7	QY 414 LysLysLeuLeuIleuProlleAlaItyAlaLysSerIeuaValProProAsnArgThr 433	
COMMENT	Location/Qualifiers	Db 122 RAGAGCCTCTGACCTGGCCATTGCTAGTGGCCCTAAGTCACT 63	
KEYWORDS	1. 781	QY 434 SerSerProLeuAlaLysThr 440	
ORGANISM	/organism="Solanum tuberosum"	Db 62 TCITCCCCACTAGAAAGACA 42	
CULTIVAR	/cultivar="Kennebec or Binjte"		
TISSUE	/db_xref="STMH067"		
CLONE	/clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"		
LAB HOST	/lab_host="SOLR"		
NOTE	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XbaI; supplier: Combination of untreated and Phytophthora		

RESULT 5
B0046203 LOCUS EST 29-MAR-2002
DEFINITION EST595321 P. infestans-challenged potato leaf, incompatible reaction Solanum tuberosum cdNA clone BPL14E21 5' end, mRNA

SEQUENCE	sequence.	QY	147	TyrAspPargCysGlyGluValCysAlaGluTyraLysThrPheArgLeuGlyThrLys	166
BQ046203.1	GR:19820189	Db	245	TATGATCGTGTGGAAAGTAGTGAGATGCTGAAGACATTACTAGAACCATG	304
KEYWORDS	EST, Potato.	QY	167	LeuMetThrProGluArgArgAlaIleTrpAlaIleTyraLysCysArgArgThr	186
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eu dicots; Asteridae; euasterids I; Solanales; Solanum.	Db	305	CTAATGACTCCAGACAAGAGGTATCGGCCATATATGTTGTCAGGAGAAC	364
ORGANISM	1 (bases 1 to 751)	QY	187	AspGluLeuValAspGlyProGlnAlaSerHisIleThrProGlnAlaLeuAspPargTrp	206
REFERENCE	Zhang, P., Hernandez, M., Torngquist, C. E., Wirtz, U., Loukotianov, A., Rangel, P., Habelich, G. T., Karanycheva, S. A., Tsai, J., Chiemingo, A., Bougrini, O., Biebell, C. R., Ronning, C. M., Helgesson, J., and Baker, B., Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, incompatible Interaction (2002) Unpublished (2002)	Db	365	GATGGCTCTGTTGATGGCCCTTAATGATCACATACACTCCACAAACCTTATGATGGTTG	424
AUTHORS	Contact: Research Genetics, Libraries Division Tel: 1-800-711-6195 Email: cdna@resgen.com	QY	207	GlutnArgLeuGluAspPhePheSerGlyArgProPheAspMetLeuAspAlaLeu	226
TITLE	For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com	Db	425	GAGGCCAGGGCTGGAAAGATTTCAACGGGGCATTGATAATGCTTGATGCACTGTTA	484
JOURNAL	Seq primer: T3.	QY	227	SerAspThrValSerArgPheProValAspPheGlnProleArgAspMetIleGluGly	246
COMMENT	1. 751 /organism="Solanum tuberosum" /cultivar="Kennebec" /db_xref="NP_011413" /clone_id="P_E21" /clone_lb="P. infestans-challenged potato leaf" /incompatible_reaction" /tissue_type="leaf" /dev_stage="6 week old" /lab_host="SOIL" /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: UC Berkeley, PGEC; sequencing: The Institute for Genomic Research. Whole plants were challenged with 450,000 sporangia/ml P. infestans isolate US-1 (US#0501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Kataldin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."	Db	485	TCCGTAATCTGTTCAAATTCCTGTGATATTAGCATTCAGAGATATGGTGAAGGA	544
FEATURES	Location/Qualifiers	QY	247	MetArgMethAspLeuTrpLysSerArgTyrlsThrPheAspGluLeuTyreLeutnTyrCys	266
source	1.	Db	545	ATGCCTATGGACTTGTGGAAATCCAGATACAAACATCTGTGAACTATATCTATATTGT	604
LOCUS	/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: UC Berkeley, PGEC; sequencing: The Institute for Genomic Research. Whole plants were challenged with 450,000 sporangia/ml P. infestans isolate US-1 (US#0501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Kataldin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."	DEFINITION	765	bP mRNA	EST 22-JAN-2002
BASE COUNT	219 a 119 c 199 g 214 t	QY	306	InLeuThrAsnLeuArgAspVal	314
ORIGIN	9.55e-130	Length:	751		
Alignment Scores:	9.55e-130	Matches:	225		
Pred. No.:	1136.00	Conservative:	11		
Score:	94.40%	Mismatches:	12		
Percent Similarity:	90.00%	Indels:	3		
Best Local Similarity:	50.00%	Gaps:	0		
Query Match:	14				
DB:					
US-09-847-081B-2 (1-440) X BQ046203 (1-751)					
QY	67	AlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysSerThrPheSer	86		
Db	5	GCAGATTGAGATATCGTGTAGTAAAGATCAAACTAGAATGGAGGAGTTTCT	64		
QY	87	ValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSerGluLysLys	106		
Db	65	GTACACTCACTTGTGGCTAGTCCAGCNGGAGAAATGCTGTCATAGAAGAAG	124		
QY	107	ValTyAspPvalValLeuLysGlnAlaAlaLeuValLysGlnAlaLeuArgSerThrAsp	126		
Db	125	GTGTAGTGGTGTGTTGTTGAGCAGCTAGTGGCTAGTGGCTAGTGGATCTACTGAG	184		
QY	127	AspLeuGluValLysProAspIleValValProGlyAsnLeuGlyLeuLeuSerGluAla	146		
Db	185	GACATAAGTGAAGCAGGATATTGTCGCGGTAAATTGGCTTGTGAGTGAAGCA	244		
FEATURES	source	COMMENT	1.	765	Location/Qualifiers
		REFERENCE	/organism="Lycopersicon esculentum"		
		AUTHORS	/cultivar="TA196"		
			/db_xref="taxon:4081"		
			/clone="clBG46P23"		
			/clone_lib="tomato breaker fruit"		
			/tissue_type="Pericarp"		

/dev_stage="breaker"	
/lab_host="SORR"	
/note="Vector: pBluescriptSKM/Cuadadt; Site_1: Ecor1;	
Site_2: xhol; supplier: Boyce Thompson Institute;	
sequencing: The Institute for Genomic Research; Fruit	
were harvested at the breaker stage (first sign of	
lycopene accumulation on the blossom end of fruit). Fruit	
were cut in half and the seeds and locules were discarded	
prior to freezing the pericarp.	
BASE COUNT	237 a 204 g
ORIGIN	
Alignment_Scores:	
Pred. No. : 5.45e-129	Length: 686 bp
Score: 1130.00	mRNA linear
Percent Similarity: 90.94%	EST 18-MAY-2001
Best Local Similarity: 87.40%	AW442101
Query Match: 49.78%	EST DEFINITION EST311497 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA clone CLEN21G20 5, mRNA sequence.
DB: 13	AW442101
US-09-847-081B-2 (1-440) x BM408984 (1-765)	ACCESSION AW442101.1 GI:6977352
KEYWORDS EST.	VERSION
SOURCE tomato.	VERSION
ORGANISM Lycopersicon esculentum	KEYWORDS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	ORGANISM
Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;	
Asteridae; euasterids I; Solanales; Solanaceae.	
Lycopersicon.	
REFERENCE 1 (bases 1 to 686)	AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
JOURNAL Unpublished (1999)	TITLE Generation of ESTs from tomato fruit tissue
COMMENT Contact: CUGI	COMMENT
Clemson University Genomics Institute	COMMENT
Clemson University	COMMENT
100 Jordan Hall, Clemson, SC 29634, USA	COMMENT
Email: http://www.genome.clemson.edu/orders/index.html	COMMENT
FEATURES	Location/Qualifiers
source	1. .686
Qy 128 LeuGluValAspProAspLevalProGlyAsnLysGluLeuSerGluAlaTyr 147	/organism="Lycopersicon esculentum"
Db 1 TAGAGGTGAAGCCGATATACTTTCGGGAAATTGGCTTGACTGAACCATAT 60	/cultivar="TA496"
Qy 148 AspArgCysGlyGluValCysAlaGluTyroAlaLysThrPhyLeuGlyThrLysLeu 167	/db_xref="taxon:4081"
Db 61 GATAGCTGTGTGAGTATGCAAGATGCAAGATGCAAGATGCAAGATGCAACTATGCAACTATGCA 120	/clone_libr="CLEN21G20"
Qy 168 MetIleProGluValGargGalaIleTrpAlaIleTyrValIlePheAspIleGly 187	/tissue-type="pericarp"
Db 121 ATGACTCCCGAGAGAGAAGGGCTATCTGGCAATATAGTATGGCAAT 200	/dev_stage="red ripe (7-20 days post-breaker)"
Qy 188 GluLeuValAspGlyProAsnAlaSerHisIleIleIleProGlnAlaLeuAspIleTrpGlu 207	/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2: XbaI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
Db 181 GAACTGTGATGGGCCAACGCACATATAATTACCCGAGCTTAGATAGTGGAA 240	
Qy 208 ThrArgLeuGluAspIlePheSerDtryArgPropeAspMetLeuAspAlaAlaLeuSer 227	
Db 241 AATAGCTAGAAGATTTCACTTCCAGTGTATACTAGCCATTAGAGATATGATTGANGAATG 300	
Qy 228 AspTrpValSerArgPheProAlaAspIleGlnProPheArgAspMetIleGluGlyMet 247	
Db 301 GATACAGTTCTAACATTCCAGTGTATACTAGCCATTAGAGATATGATTGANGAATG 360	
Qy 248 ArgMetAspLeutPheSerArgTrpLysLysThrPheAspAluLeutYrLeutYrCystYr 267	
Db 361 CGTATGGACTTGAGAAATCAGGATAACAAACTGAGACTTACCTTATGTTAT 420	
Qy 268 TyrValAlaGlyIleThrValGlyLeuMetSerValProValAspIleAlaProGluUser 287	BASE COUNT
Db 421 TATGTGCTGGTACCGTGGTTGACTGTTGAGTGTGATGACTGTTGCTGTCC 480	ORIGIN
Qy 288 LysAlaIleThrGluUserValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAspGlnLeu 307	Alignment Scores:
Db 481 AAGGCRACACAGAGCTATATAATGCTGCTTGGCTGCAATTCGAAATCAATTAA 540	Pred. No.: 3.17e-125
Qy 308 ThrAsnIleLeuGluAspGlyIleGluAspAlaArgGlyArgValTyrLeuProGln 327	Length: 686
Db 541 ACTACATACTCAGGATGCTGGGAGATGCCGAGGGAAAGTACTCTCTCAA 600	Matches: 209
Qy 328 AspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle-PheAlaGlyArgValThrAs 347	Conservative: 9
Db 601 GATGATTAGCACGGCAGTCTTGTGAATATTTCCTGGAAAGGGTGACCGA 660	Mismatches: 10
Qy 347 PheAspPheAsnPheMetIleGlnArgAlaArgLySphpheAspGluSe 367	InDel: 0
Db 661 TAAATGGAGATCTATGAGAACAA--TACTAGGCCAAGAAAGCTTGTGAGCA 717	Gaps: 0
Qy 367 rGluIysGlyValIrhGluLeuAspSerAlaSerArgTrp 380	US-09-847-081B-2 (1-440) x AW442101 (1-686)
Db 718 GAGAAAGCT---GACAGATGCTCACTAGTGAATGCTA 754	Qy 108 TyrAspAlvLeuLeuLysGlnAlaAlaLeuValGlyIleGluArgSerThrAsp 127
Qy 268 TyrValAllysThrPhyTyrIleGluAlaLeuLeuArgSerThrAsp 127	Db 2 TATGAGTGTGTTGGCTGAGGCAACTGAGATCTACCAATGAG 61
Db 421 LeuGluValLysProSpIlePheValValProGlyAsnIleGluLeuSerGluAlaTyr 147	Qy 128 LeuGluValLysProSpIlePheValValProGlyAsnIleGluLeuSerGluAlaTyr 147
Qy 480 LysAlaIleThrGluUserValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAspGlnLeu 307	Db 62 TATGAGTGTGAGCCGATATACTATCCTGAGCTTGTGAGTGTAGCATAT 121
Db 540 LysAlaIleThrGluUserValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAspGlnLeu 307	Qy 148 AspArgCysGlyIleGluAlaGlyIleGluAlaLeuLeuArgSerThrAsp 187
Qy 600 LysAlaIleThrGluUserValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAspGlnLeu 307	Db 122 GATAGGTGTGTTGAACTATGGCAGTAACTGGACTATCTGCTA 181
Db 660 LysAlaIleThrGluUserValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAspGlnLeu 307	Qy 168 MetThrProGluArgArgAlaIleIleTrpAlaIleIleTrpCysArgArgThrAsp 187
Db 720 LysAlaIleThrGluUserValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAspGlnLeu 307	Db 182 ATGACTCCGGAGAGAGGGCTATCTGGGAAATATGATGGCTCAGAGAACAGAT 241

sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp.*

BASE COUNT 217 a 114 c 173 g 178 t

ORIGIN

Alignment Scores:

Pred. No.:	3.02e-123	Length:	682
Score:	1083.00	Matches:	207
Percent Similarity:	94.71%	Conservative:	8
Best Local Similarity:	91.19%	Mismatches:	12
Query Match:	47.71%	Indels:	0
DB:	13	Gaps:	0

US-09-847-081B-2 (1-440) x BM409200 (1-682)

QY 188 GlutLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGlu 207

Db 242 GAACTTGTTGATGCCAAACGGCATATAATTACCCGGCAGCCATTAGATAGGTGGAA 301

QY 208 ThrArgLeuGluAspIleSerGlyArgProPheAspMetLeuAspAlaAlaLeuSer 227

Db 302 AATGGCAGAAGATGTTCAATGGGGCCATTGACATGCTGAATGGCTTC 361

QY 228 AspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMet 247

Db 362 GAPACAGTTCAACTTCCAGITGATATTGAGATAATGATTGAGGATG 421

QY 248 ArgMetAspLysPheLysSerArgTyiLysThrPheAspGluLeuTyiLeuTyiCystYr 267

Db 422 CGTAGGACTTGAAATCGAGATAACAAACTTCGCGAACTATACCTTATTGTTAT 481

QY 268 TyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGluSer 287

Db 482 TATGTTGGTACGGTTGGTGTATGTTGGTGTCCATTATGGTTATGCCCTGATACA 541

QY 288 LysAlaIthrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeu 307

Db 542 RAGGCAAACACAGAGGTTATATGCTGCTGGGATGCAATTAATCAATA 601

QY 308 ThrAsnIleLeuArgAspValGlyIleAspAlaArgArgGlyArgValTyiLeuProGln 327

Db 602 ACTAACAACTGAGAGTGGAGAGATGCCAGAGAGATGCCAGAGAGTGCCTACTTGCCCTCAA 661

QY 328 AspGluLeuAlaGlnAlaGlyLeu 335

Db 662 GATGAAATTACCCAGGGCGGGCTTA 685

RESULT 8

LOCUS BM409200 682 bp mRNA linear EST 22-JAN-2002

DEFINITION EST583527 tomato breaker fruit Lycopersicon esculentum cDNA clone CLEG4JU1 5' end, mRNA sequence.

ACCESSION BM409200

VERSION 1.1.8260830

SOURCE EST.

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE Alcalá,J., Vrehlov,J., White,R., Vision,T., Karanicheva,S.A., Tsai J., Bougri,O., Kiriness,E., Utterback,T., Van Aken,S., Ronning C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002) Unpublished (2002)

JOURNAL Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics Institute

Seq Primer: T3.

Location/Qualifiers

- .682 "Lycopersicon esculentum"
- /organism="Lycopersicon esculentum"
- /cultivar="TOM498"
- /db_xref="taxon:4081"
- /clone_id="tomato breaker fruit"
- /tissue_type="Pericarp"
- /dev_stage="breaker"
- /lab_host="SOLR"
- /note="Vector: pBluescriptSKmICUadapt; Site_1: EcoRI; Site_2: XbaI; supplier: Boyce Thompson Institute"

FEATURES

source

1. .682 "Lycopersicon esculentum"

/cultivar="TOM498"

/clone_id="tomato breaker fruit"

/tissue_type="Pericarp"

/dev_stage="breaker"

/lab_host="SOLR"

/note="Vector: pBluescriptSKmICUadapt; Site_1: EcoRI; Site_2: XbaI; supplier: Boyce Thompson Institute"

RESULT 9

AW42407 LOCUS AW42407 EST 18-MAY-2001

DEFINITION EST311803 tomato fruit red ripe, TAMU Lycopersicon esculentum CDNA clone CLEN22L14 5', mRNA sequence.

ACCESSION AW442407

VERSION AW442407 GI:6977658

KEYWORDS	tomato.
SOURCE	Lycopersicon esculentum;
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicots; core eudicots;
REFERENCE	Asteridae; eustemids I; Solanales; Solanaceae; Solanum;
AUTHORS	Alcalá, J., Vrabalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.J.
TITLE	Generation of ESTs from tomato fruit tissue
JOURNAL	Unpublished (1999)
COMMENT	Contact: CUGI Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html
FEATURES	5 prime sequence.
source	1. .672 /organism="Lycopersicon esculentum" /cultivar="TA86". /db_xref="taxon:4081". /clone_id="CLEN2214". /clone_lib="tomato fruit red ripe, TAMU" /tissue_type="pericarp" /dev_stage="red ripe (7-20 days post-breaker)" /note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2: XbaI, supplier: Giovannoni, Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
BASE COUNT	212 a 112 c 170 g 178 t
ORIGIN	
Alignment Scores:	
Pred. No.:	6.79e-122
Score:	1072.00
Percent Similarity:	95.07%
Best Local Similarity:	91.93%
Query Match:	47.22%
Db:	10
	Gaps: 0
US-09-847-081B-2 (1-440) x AW442407 (1-672)	
Qy	160 ThphetyltryuglyThrlsLeuMetthrProGluArgArgGalaIleThrPAlaIle 179
Db	3 ACGTTPACTTAGAATCTAGCTATACTGACCCGAGAGAAAGGCATATAATTACA 62
Qy	180 TyrValTrpCysArgArgThrAspGluLeuValAspGlyProAspAlaSerHisIleThr 199
Db	63 TAGTATGGTCAGAGAACATGACTGTTGATGCTATGATGCGCAATA 122
Qy	200 ProGlnAlaLeuAspArgTrpGluLthArgLeuGluAspIlePheserGlyArgProPhe 219
Db	123 CGGGCAGCCCTAGATGGGGAAAATAGGCTAGAGATGTTCAATGGGGCATT 182
Qy	220 AspMetLeuAspAlaIleUserAspThrValSerArgPheProValAspIleGlnPro 239
Db	183 GACATGCTGATGGCTGCTGTCGATACGTTCACTTCCAGTGATATTAGCCA 242
Qy	240 PheArgAspMetIleGluGlyMetArgMetAspLeuPheSerArgPheLysThrPhe 259
Db	243 TTCAAGATGATGATTGATGAGATGCTAGATGTTCAATGGGGTATGAGTGTCCA 302
Qy	260 AspGluLeuItyLeuItyCystrytryvalAlaglyThrValGlyLeuMetSerValPro 279
Db	303 GACGAACTATACCTTTATTTGTTATGTTGCTGGTGTGGTGTGATGAGTGTCCA 362

Db	542	AAGGGCTGACAGAATTGAGCTCAGCTAGATCCGTATGGCATCTTGGCTTG 601	Qy	105	LysLysValTyrAspValLeuLysGlnAlaAlaLeuValLysArgGlnLeuArgSer 124
Qy	389	TyrArgLysIleLeuAspGluIleGluAlaLysAspTyraAlaAsnDherHArgAla 408	Db	240	AAAAGCTGTATGAGCTGTATTGAAACGGCAGCTTAGTAAGGCCATCTGATACT 299
Db	602	TACCCGCAATACTAGTAGTTGAGCTTGAAGCCAAATGACTAACACAACCTCACAAAGAGCA 661	Qy	125	ThrasAspLeuGluValLysProAspIleValAlProGlyAsnLeuGlyLeuLeuSer 144
Qy	409	TyralValSerLys 412	Db	300	ACTGAGACATGAGAAGTGAAGCCGAAATTGGCTGAAATTGGCTGTTGAGT 359
Db	662	TATCTGAGCAA 673	Qy	145	GluAlaTyrAspArgCysGlyluValCysAlaGluTyrAlaLysThrPheTyrLeuGly 164
RESULT 12			Db	360	GAAGCATATGATCGTGTGGAAAGTAGTCAGAGTATCTACTAGA 419
LOCUS	BG351357	677 bp mRNA linear EST 01-MAR-2001	Qy	165	ThrLysLeuMetThrProGluArgArgAlaIleTPalIleTerTyrValTpcysArg 184
DEFINITION	104A12	Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA sequence.	Db	420	ACCATGCTAAATGACTCCAGACAGAAAGAGCTATCAGGGCATATATGTTGGCAGG 479
ACCESSION	BG351357	EST: BG351357.1 GI:13180099	Qy	185	ArgThrAspGluValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuHsp 204
KEYWORDS			Db	480	AGAACTGATGAGCTTGTGATGCCPAATGATCACACAAGCTTATG 539
SOURCE			Qy	205	ArgTrpGluIleThrArgLeuAspIleSerGlyArgProHeAspMetLeuAspAla 224
ORGANISM			Db	540	AGTGGGAGGGCAGGGCTGGAAAGATATTTCAAGGGCGCCATATGATGCTGATGCA 549
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.			Qy	225	AlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIle 244
REFERENCE			Db	600	GCTTAACCGGACTGTTCCARATTTCCTGTCGATATTAGCCTTCAGAGATACTGGT 659
AUTHORS			Qy	245	GluGlyNetArgMetAsp 250
TITLE			Db	660	GAAGGAATGCGTATGGAC 677
JOURNAL			RESULT 13		
COMMENT			BM412533	634 bp mRNA linear EST 22-JAN-2002	
			DEFINITION	EST588660	tomato breaker fruit Lycopersicon esculentum cdNA clone
			ACCESSION	BM412533	CLEG6014 5, end, mRNA sequence.
			VERSION	BM412533.1	GI:18264163
			KEYWORDS	EST.	
			SOURCE		tomato.
			ORGANISM		Lycopersicon esculentum
					Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
FEATURES	source		REFERENCE		
			AUTHORS	Alcalá,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougré,O., Kirkinis,E., Utterbeck,T., Van Aken,S., C.M. Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.	
			TITLE		
			JOURNAL		Generation of ESTs from tomato fruit tissue, breaker stage (2002)
			COMMENT		Unpublished (2002)
					Contact: CUGI
					Clemson University Genomics Institute
					Clemson University
					100 Jordan Hall, Clemson, SC 29634, USA
					Email: http://www.genome.clemson.edu/orders/index.html
					This clone is available through the Clemson University Genomics Institute
BASE COUNT	192 a	102 c 198 g 185 t	FEATURES	source	
ORIGIN					1 (bases 1 to 634)
					/organism="Lycopersicon esculentum"
Alignment Scores:					/cultivar="TA496"
Pred. No :		4.31e-113			/db_xref="TA496"
Score:		1001.00	Length:	677	/clone="CLEG6014"
Percent Similarity:		91.15%	Matches:	195	/clone.lib="tomato breaker fruit"
Best Local Similarity:		86.38%	Conservative:	11	/tissue_type="Pericarp"
Query Match:		44.10%	Mismatches:	20	/dev_stage="breaker"
DB:			Indels:	1	/lab_host="SOLR"
			Gaps:	0	/note="Vector: Lambda ZAP"
US-09-847-081B-2 (1-440) x BG351357 (1-677)					/site_2="Supplier: Boyce Thompson Institute; Site_1: EcoRI; Site_2: Choi; supplier: Boyce Thompson Institute;"
Qy	25	AspSerValArgGluIysArgNargValPheValSerArgPheLeuAlaArgAspArg 44			
Db	1	GATTCAGTCGAAAGGGAAACGGGG-TTGGATCATCCAGGTCCATCTCGAATGG 59			
Qy	45	AspLeuMetTrpAsnGlyArgIleLysGlyIysGlyArgGlnDargTrpAsnPheGlySer 64			
Db	60	AATTCGATGGAAAGGAGATCAAGAAGGGAGCAAGGTGAAATTGGCTT 119			
Qy	65	LeuIleAlaAspProAspTyrSerCysLeuGlySerArgThrGlyLysGlySerThr 84			
Db	120	TAAATGCGATTTGAGATTTGGTGTAGAGATCAAGACTGAGATACTGAAAGGAGT 179			
Qy	85	PheservalGlnSerSerIvalAlaSerProAlaGlyIleValSerThrValSerGlu 104			
Db	180	TTTCCTGACAGTCAGTGGCTAGTGGCTGATCCAGCTGAGAATGGCTGTCATCAGAG 239			

sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicum.

Niemann, W., Faseli, C.M., Mai-Luu, S.B., Giovannoni, J.J., and Lai						
"S. D.						
Alignment Scores:						
aligned. No. :	1-21e-112	Length:	634			Generation of ESTs from tomato fruit tissue, breaker stage
Score:	997.00	Matches:	194			Unpublished (2000)
Percent Similarity:	94.31%	Conservative:	5			Contact: CUGI
Best Local Similarity:	91.94%	Mismatches:	12			Clemson University Genomics Institute
Query Match:	43.92%	Indels:	1			100 Jordan Hall, Clemson, SC 29634, USA
:	13	Gaps:	0			Email: http://www.genome.clemson.edu/orders/index.html
-	-09-847-081B-2 (1-440) x BM412533 (1-634)					5 prime sequence.
FEATURES						Location/Qualifiers
source						1. 600
						/organism="Lycopersicon esculentum"
						/cultivar="T495"
						/db_xref="taxon:4081"
						/clone="cLEG36H12"
						/clone_lib="tomato breaker fruit, TIGR"
						/tissue_type="Pericarp"
						/dev_stage="breaker"
						/lab_host="SOLR"
						/note="vector: PBluescriptSKMCuadapt; Site:1: EcoRI; Site:2: XbaI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
BASE COUNT						178 a 99 c 157 g 166 t
ORIGIN						
Alignment Scores:						
Pred. No. :	1-42e-110	Length:	600			
Score:	980.00	Matches:	185			
Percent Similarity:	95.98%	Conservative:	6			
Best Local Similarity:	92.96%	Mismatches:	8			
Query Match:	43.17%	Indels:	0			
DB:	10	Gaps:	0			
US-09-847-081B-2 (1-440) x BE460889 (1-600)						
Qy	137 ProGlyAsnLeuGlyLeuLeuSerGluAlaTyrsArgPcysGlyGluValCysAlaGlu					
Db	3 CGGGGAATTTGGCTGTGTTAGTGAGTCATATGATGGTGTGAGTCAGAG					
Qy	157 TyrAlaLysThrPhetYLeucGlyThrLysLeuMetThrProGluAFArgArgA9AlaAlle					
Db	63 TATGCAAAGACTTGTAACTTAGGTTACTTGAACATGCTTAATGCTGTTGAGTCAGAG					
Qy	177 TrpAlaLysThrValTrpCysArgA9GlyThrAspGluLeuValAspGly1ProAspAlaSer					
Db	123 TGGGAAATAPATGTTATGGTGCAGAGACAGATGAACTTGTGAAAGCTCAAAAGCATA					
Qy	197 HisIleThrProGlnAlaLeuAspArgGlyGluThrArgLeuGluAspIlePheserGly					
Db	183 TATATAACCCGGCAAGCTTGTAGATAGTGGGAAAATGGCTGAAAGCTGTTCAATGGG					
Qy	217 ArgProProAspMetLeuAspAlaLeuUserAspThrValSerArgPheProValAsp					
Db	243 CGGCATTGACATGCTGAGCTTGTAGATAGTGGGAAAATGGCTGAAAGCTGTTCAATGG					
Qy	237 IleGlnProProAspMetIleGluGlyMetArgMetAspLeuTriPlysSerArgPheProValAsp					
Db	303 ATTACCCATTGACGAACTATACCTTATGACTGAGATGAAATCGAGATAC					
Qy	257 LysInProAspGluLeuIleTyroLeutYcystYrrValAlaGlyThrValGlyLeuMet					
Db	363 AAAACTTCGACGAACTATACCTTATGACTGAGATGAAATCGAGATAC					
Qy	277 SerValProValMetGlyIleIaProGluUserIysAlaThrThrGluSerValTyrAsn					
QXUS	BE460889 600 bp, mRNA linear EST 18-MAY-2001					
DEFINITION	EST412308 tomato breaker fruit, TIGR Lycopersicon esculentum CDNA clone cLEG36H12, mRNA sequence.					
VERSION	BE460889 EST					
KEYWORDS						
ORGANISM	Lycopersicon esculentum					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
RESULTS	AAACAATA-CATAGGGCAGAAAGTCTTGTAT 632					
DISCUSSION	CTATCGGATGAGATATATGCTGGAGGTGACCCATAATGGAGAACATCTTATGAG 600					
TERMINATOR	LYSGIINIEGInArgAlaArgGlySpheAsp 365					
EST	AAACAATA-CATAGGGCAGAAAGTCTTGTAT 632					
SOURCE	BE460889.1 GI:9505191					
ORGANISM	Lycopersicon esculentum					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
RESULTS	AAACAATA-CATAGGGCAGAAAGTCTTGTAT 632					
DISCUSSION	CTATCGGATGAGATATATGCTGGAGGTGACCCATAATGGAGAACATCTTATGAG 600					
TERMINATOR	LYSGIINIEGInArgAlaArgGlySpheAsp 365					
SOURCE	BE460889.1 GI:9505191					
ORGANISM	Lycopersicon esculentum					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						

```

/clone="cLELG8H5"
/clone.lib="tomato breaker fruit, TIGR"
/tissue.type="Pericarp"
/dev.stage="breaker"
/lab.host="SOLR"
/note="vector: pBlueScriptSKMquadrant; Site_1: Ecop1;
Site_2: Xhol; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
191 a 101 c 164 g 167 t

```

Alignment Scores:
Pred. No.:
Score:
Percent Similarity
Best Local Similar
Query Match:
DB: